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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/904,099

DATE: 11/06/2001
TIME: 11:58:40

Input Set : A:\10602-013-999.txt
Output Set: N:\CRF3\11062001\I904099.raw

3 <110> APPLICANT: Shankar, Geetha
5 Munning, Jason N
7 Spencer, Juliet V
9 <120> TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS
11 <130> FILE REFERENCE: 10602-013-999
13 <140> CURRENT APPLICATION NUMBER: 09/904,099
15 <141> CURRENT FILING DATE: 2001-07-11
17 <160> NUMBER OF SEQ ID NOS: 38
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
23 <211> LENGTH: 382
25 <212> TYPE: PRT
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1
31 Met Gly Pro Thr Ser Val Pro Leu Val Lys Ala His Arg Ser Ser Val
32 1 5 10 15
33 Ser Asp Tyr Val Asn Tyr Asp Ile Ile Val Arg His Tyr Asn Tyr Thr
34 20 25 30
35 Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu Thr
36 35 40 45
37 Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu Glu Asn Ile
38 50 55 60
39 Phe Val Leu Leu Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro Met
40 65 70 75 80
41 Tyr Tyr Phe Ile Gly Asn Leu Ala Leu Ser Asp Leu Leu Ala Gly Val
42 85 90 95
43 Ala Tyr Thr Ala Asn Leu Leu Ser Gly Ala Thr Thr Tyr Lys Leu
44 100 105 110
45 Thr Pro Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala Leu
46 115 120 125
47 Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr Ile
48 130 135 140
49 Thr Met Leu Lys Met Lys Leu His Asn Gly Ser Asn Asn Phe Arg Leu
50 145 150 155 160
51 Phe Leu Leu Ile Ser Ala Cys Trp Val Ile Ser Leu Ile Leu Gly Gly
52 165 170 175
53 Leu Pro Ile Met Gly Trp Asn Cys Ile Ser Ala Leu Ser Ser Cys Ser
54 180 185 190
55 Thr Val Leu Pro Leu Tyr His Lys His Tyr Ile Leu Phe Cys Thr Thr
56 195 200 205
57 Val Phe Thr Leu Leu Leu Ser Ile Val Ile Leu Tyr Cys Arg Ile
58 210 215 220
59 Tyr Ser Leu Val Arg Thr Arg Ser Arg Arg Leu Thr Phe Arg Lys Asn
60 225 230 235 240
61 Ile Ser Lys Ala Ser Arg Ser Ser Glu Lys Ser Leu Ala Leu Leu Lys
62 245 250 255
63 Thr Val Ile Ile Val Leu Ser Val Phe Ile Ala Cys Trp Ala Pro Leu

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64 260 265 270
 66 Phe Ile Leu Leu Leu Leu Asp Val Gly Cys Lys Val Lys Thr Cys Asp
 67 275 280 285
 68 Ile Leu Phe Arg Ala Glu Tyr Phe Leu Val Leu Ala Val Leu Asn Ser
 69 290 295 300
 70 Gly Thr Asn Pro Ile Ile Tyr Thr Leu Thr Asn Lys Glu Met Arg Arg
 71 305 310 315 320
 72 Ala Phe Ile Arg Ile Met Ser Cys Cys Lys Cys Pro Ser Gly Asp Ser
 73 325 330 335
 74 Ala Gly Lys Phe Lys Arg Pro Ile Ile Ala Gly Met Glu Phe Ser Arg
 75 340 345 350
 76 Ser Lys Ser Asp Asn Ser Ser His Pro Gln Lys Asp Glu Gly Asp Asn
 77 355 360 365
 78 Pro Glu Thr Ile Met Ser Ser Gly Asn Val Asn Ser Ser Ser
 79 370 375 380
 81 <210> SEQ ID NO: 2
 83 <211> LENGTH: 378
 85 <212> TYPE: PRT
 87 <213> ORGANISM: Homo sapiens
 89 <400> SEQUENCE: 2
 91 Met Ala Thr Ala Leu Pro Pro Arg Leu Gln Pro Val Arg Gly Asn Glu
 92 1 5 10 15
 93 Thr Leu Arg Glu His Tyr Gln Tyr Val Gly Lys Leu Ala Gly Arg Leu
 94 20 25 30
 95 Lys Glu Ala Ser Glu Gly Ser Thr Leu Thr Thr Val Leu Phe Leu Val
 96 35 40 45
 97 Ile Cys Ser Phe Ile Val Leu Glu Asn Leu Met Val Leu Ile Ala Ile
 98 50 55 60
 99 Trp Lys Asn Asn Lys Phe His Asn Arg Met Tyr Phe Phe Ile Gly Asn
 100 65 70 75 80
 101 Leu Ala Leu Cys Asp Leu Leu Ala Gly Ile Ala Tyr Lys Val Asn Ile
 102 85 90 95
 103 Leu Met Ser Gly Lys Lys Thr Phe Ser Leu Ser Pro Thr Val Trp Phe
 104 100 105 110
 105 Leu Arg Glu Gly Ser Met Phe Val Ala Leu Gly Ala Ser Thr Cys Ser
 106 115 120 125
 107 Leu Leu Ala Ile Ala Ile Glu Arg His Leu Thr Met Ile Lys Met Arg
 108 130 135 140
 109 Pro Tyr Asp Ala Asn Lys Arg His Arg Val Phe Leu Leu Ile Gly Met
 110 145 150 155 160
 111 Cys Trp Leu Ile Ala Phe Thr Leu Gly Ala Leu Pro Ile Leu Gly Trp
 112 165 170 175
 113 Asn Cys Leu His Asn Leu Pro Asp Cys Ser Thr Ile Leu Pro Leu Tyr
 114 180 185 190
 115 Ser Lys Lys Tyr Ile Ala Phe Cys Ile Ser Ile Phe Thr Ala Ile Leu
 116 195 200 205
 117 Val Thr Ile Val Ile Leu Tyr Ala Arg Ile Tyr Phe Leu Val Lys Ser
 118 210 215 220
 119 Ser Ser Arg Lys Val Ala Asn His Asn Asn Ser Glu Arg Ser Met Ala

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120 225 230 235 240
122 Leu Leu Arg Thr Val Val Ile Val Val Ser Val Phe Ile Ala Cys Trp
123 245 250 255
124 Ser Pro Leu Phe Ile Leu Phe Leu Ile Asp Val Ala Cys Arg Val Gln
125 260 265 270
126 Ala Cys Pro Ile Leu Phe Lys Ala Gln Trp Phe Ile Val Leu Ala Val
127 275 280 285
128 Leu Asn Ser Ala Met Asn Pro Val Ile Tyr Thr Leu Ala Ser Lys Glu
129 290 295 300
131 Met Arg Arg Ala Phe Phe Arg Leu Val Cys Asn Cys Leu Val Arg Gly
132 305 310 315 320
133 Arg Gly Ala Arg Ala Ser Pro Ile Gln Pro Ala Leu Asp Pro Ser Arg
134 325 330 335
135 Ser Lys Ser Ser Ser Asn Asn Ser Ser His Ser Pro Lys Val Lys
136 340 345 350
137 Glu Asp Leu Pro His Thr Asp Pro Ser Ser Cys Ile Met Asp Lys Asn
138 355 360 365
139 Ala Ala Leu Gln Asn Gly Ile Phe Cys Asn
140 370 375
142 <210> SEQ ID NO: 3
144 <211> LENGTH: 391
146 <212> TYPE: PRT
C--> 148 <213> ORGANISM: Artificial

150 <220> FEATURE:
152 <223> OTHER INFORMATION: Description of artificial sequence: Chimeric Edg receptor
154 <400> SEQUENCE: 3
156 Met Gly Pro Thr Ser Val Pro Leu Val Lys Ala His Arg Ser Ser Val
157 1 5 10 15
158 Ser Asp Tyr Val Asn Tyr Asp Ile Ile Val Arg His Tyr Asn Tyr Thr
159 20 25 30
160 Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu Thr
161 35 40 45
162 Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu Glu Asn Ile
163 50 55 60
164 Phe Val Leu Leu Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro Met
165 65 70 75 80
166 Tyr Tyr Phe Ile Gly Asn Leu Ala Leu Ser Asp Leu Leu Ala Gly Val
167 85 90 95
168 Ala Tyr Thr Ala Asn Leu Leu Ser Gly Ala Thr Thr Tyr Lys Leu
169 100 105 110
170 Thr Pro Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala Leu
171 115 120 125
172 Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr Ile
173 130 135 140
174 Thr Met Leu Lys Met Lys Leu His Asn Gly Ser Asn Asn Phe Arg Leu
175 145 150 155 160
176 Phe Leu Leu Ile Ser Ala Cys Trp Val Ile Ser Leu Ile Leu Gly Gly
177 165 170 175
178 Leu Pro Ile Met Gly Trp Asn Cys Ile Ser Ala Leu Ser Ser Cys Ser

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Input Set : A:\10602-013-999.txt

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| | | | | |
|-----|---|-------------------------|-----|-----|
| 179 | 180 | 185 | 190 | |
| 180 | Thr Val Leu Pro Leu Tyr His Lys His Tyr Ile Leu Phe Cys Thr Thr | | | |
| 181 | 195 | 200 | 205 | |
| 183 | Val Phe Thr Leu Leu Leu Ser Ile Val Ile Leu Tyr Cys Arg Ile | | | |
| 184 | 210 | 215 | 220 | |
| 185 | Tyr Ser Leu Val Arg Thr Arg Ser Arg Arg | Leu Thr Phe Arg Lys Asn | | |
| 186 | 225 | 230 | 235 | 240 |
| 187 | Ile Ser Lys Ala Ser Arg Ser Ser Glu Lys Ser Leu Ala Leu Leu Lys | | | |
| 188 | 245 | 250 | 255 | |
| 189 | Thr Val Ile Ile Val Leu Ser Val Phe Ile Ala Cys Trp Ala Pro Leu | | | |
| 190 | 260 | 265 | 270 | |
| 191 | Phe Ile Leu Leu Leu Asp Val Gly Cys Lys Val Lys Thr Cys Asp | | | |
| 192 | 275 | 280 | 285 | |
| 193 | Ile Leu Phe Arg Ala Glu Tyr Phe Leu Val Leu Ala Val Leu Asn Ser | | | |
| 194 | 290 | 295 | 300 | |
| 196 | Gly Thr Asn Pro Ile Ile Tyr Thr Leu Thr Ser Lys Glu Met Arg Arg | | | |
| 197 | 305 | 310 | 315 | 320 |
| 198 | Ala Phe Phe Arg Leu Val Cys Asn Cys Leu Val Arg Gly Arg Gly Ala | | | |
| 199 | 325 | 330 | 335 | |
| 200 | Arg Ala Ser Pro Ile Gln Pro Ala Leu Asp Pro Ser Arg Ser Lys Ser | | | |
| 201 | 340 | 345 | 350 | |
| 202 | Ser Ser Ser Asn Asn Ser Ser His Ser Pro Lys Val Lys Glu Asp Leu | | | |
| 203 | 355 | 360 | 365 | |
| 204 | Pro His Thr Asp Pro Ser Ser Cys Ile Met Asp Lys Asn Ala Ala Leu | | | |
| 205 | 370 | 375 | 380 | |
| 206 | Gln Asn Gly Ile Phe Cys Asn | | | |
| 207 | 385 | 390 | | |

209 <210> SEQ ID NO: 4

211 <211> LENGTH: 384

213 <212> TYPE: PRT

C--> 215 <213> ORGANISM: Artificial

217 <220> FEATURE:

219 <223> OTHER INFORMATION: Description of artificial sequence: Chimeric Edg receptor

221 <400> SEQUENCE: 4

| | | | | |
|-----|---|-----|-----|----|
| 223 | Met Gly Pro Thr Ser Val Pro Leu Val Lys Ala His Arg Ser Ser Val | | | |
| 224 | 1 | 5 | 10 | 15 |
| 225 | Ser Asp Tyr Val Asn Tyr Asp Ile Ile Val Arg His Tyr Asn Tyr Thr | | | |
| 226 | 20 | 25 | 30 | |
| 227 | Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu Thr | | | |
| 228 | 35 | 40 | 45 | |
| 229 | Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu Glu Asn Ile | | | |
| 230 | 50 | 55 | 60 | |
| 231 | Phe Val Leu Leu Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro Met | | | |
| 232 | 65 | 70 | 75 | 80 |
| 233 | Tyr Tyr Phe Ile Gly Asn Leu Ala Leu Ser Asp Leu Leu Ala Gly Val | | | |
| 234 | 85 | 90 | 95 | |
| 235 | Ala Tyr Thr Ala Asn Leu Leu Ser Gly Ala Thr Thr Tyr Lys Leu | | | |
| 236 | 100 | 105 | 110 | |
| 237 | Thr Pro Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala Leu | | | |

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Input Set : A:\10602-013-999.txt
Output Set: N:\CRF3\11062001\I904099.raw

| | | | | |
|-----|---|-----------------|-----|-----|
| 238 | 115 | 120 | 125 | |
| 239 | Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile | Glu Arg Tyr Ile | | |
| 240 | 130 | 135 | 140 | |
| 241 | Thr Met Leu Lys Met Lys Leu His Asn Gly Ser Asn Asn | Phe Arg Leu | | |
| 242 | 145 | 150 | 155 | 160 |
| 244 | Phe Leu Leu Ile Ser Ala Cys Trp Val Ile Ser Leu Ile | Leu Gly Gly | | |
| 245 | 165 | 170 | 175 | |
| 246 | Leu Pro Ile Met Gly Trp Asn Cys Ile Ser Ala Leu Ser | Ser Cys Ser | | |
| 247 | 180 | 185 | 190 | |
| 248 | Thr Val Leu Pro Leu Tyr His Lys His Tyr Ile Leu | Phe Cys Thr Thr | | |
| 249 | 195 | 200 | 205 | |
| 250 | Val Phe Thr Leu Leu Leu Ser Ile Val Ile Leu | Tyr Cys Arg Ile | | |
| 251 | 210 | 215 | 220 | |
| 252 | Tyr Ser Leu Val Arg Ser Ser Arg Lys Val Ala Asn His | Asn Asn | | |
| 253 | 225 | 230 | 235 | 240 |
| 254 | Ser Glu Arg Ser Met Ala Leu Leu Arg Thr Val Ile Ile | Val Leu Ser | | |
| 255 | 245 | 250 | 255 | |
| 256 | Val Phe Ile Ala Cys Trp Ala Pro Leu Phe Ile Leu Leu | Leu Leu Asp | | |
| 257 | 260 | 265 | 270 | |
| 258 | Val Gly Cys Lys Val Lys Thr Cys Asp Ile Leu Phe | Arg Ala Glu Tyr | | |
| 259 | 275 | 280 | 285 | |
| 261 | Phe Leu Val Leu Ala Val Leu Asn Ser Gly Thr Asn Pro | Ile Ile Tyr | | |
| 262 | 290 | 295 | 300 | |
| 263 | Thr Leu Thr Ser Lys Glu Met Arg Arg Ala Phe Phe Arg | Leu Val Cys | | |
| 264 | 305 | 310 | 315 | 320 |
| 265 | Asn Cys Leu Val Arg Gly Arg Gly Ala Arg Ala Ser Pro | Ile Gln Pro | | |
| 266 | 325 | 330 | 335 | |
| 267 | Ala Leu Asp Pro Ser Arg Ser Lys Ser Ser Ser Asn Asn | Ser Ser | | |
| 268 | 340 | 345 | 350 | |
| 269 | His Ser Pro Lys Val Lys Glu Asp Leu Pro His Thr Asp | Pro Ser Ser | | |
| 270 | 355 | 360 | 365 | |
| 271 | Cys Ile Met Asp Lys Asn Ala Ala Leu Gln Asn Gly Ile | Phe Cys Asn | | |
| 272 | 370 | 375 | 380 | |

274 <210> SEQ ID NO: 5

276 <211> LENGTH: 384

278 <212> TYPE: PRT

C--> 280 <213> ORGANISM: Artificial

282 <220> FEATURE:

284 <223> OTHER INFORMATION: Description of artificial sequence: Chimeric Edg receptor

286 <400> SEQUENCE: 5

| | | | | |
|-----|---|-------------|----|----|
| 288 | Met Gly Pro Thr Ser Val Pro Leu Val Lys Ala His Arg Ser | Ser Val | | |
| 289 | 1 | 5 | 10 | 15 |
| 290 | Ser Asp Tyr Val Asn Tyr Asp Ile Ile Val Arg His Tyr | Asn Tyr Thr | | |
| 291 | 20 | 25 | 30 | |
| 292 | Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile | Lys Leu Thr | | |
| 293 | 35 | 40 | 45 | |
| 294 | Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu | Glu Asn Ile | | |
| 295 | 50 | 55 | 60 | |
| 296 | Phe Val Leu Leu Thr Ile Trp Lys Thr Lys Phe His Arg | Pro Met | | |

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/904,099

DATE: 11/06/2001
TIME: 11:58:41

Input Set : A:\10602-013-999.txt
Output Set: N:\CRF3\11062001\I904099.raw

L:148 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:215 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:280 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:345 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:362 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:379 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:395 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:411 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:428 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:445 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:462 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:479 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:497 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:515 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:532 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:549 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:566 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:583 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:600 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:617 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:634 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:651 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:668 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:685 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:702 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:719 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:736 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:1160 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37
L:1223 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38